

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: _____ Examiner #: _____ Date: _____
 Art Unit: _____ Phone Number 30 _____ Serial Number: _____
 Mail Box and Bldg/Room Location: _____ Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

**For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

STAFF USE ONLY

STAFF USE ONLY	Type of Search	Vendors and cost where applicable
Searcher <u>D. Schreiber</u>	NA Sequence (#) _____	STN _____
Searcher Phone # <u>308-4292</u>	AA Sequence (#) <u>3</u>	Dialog _____
Searcher Location: <u>CM1 12E18</u>	Structure (#) _____	Questel/Orbit _____
Date Searcher Picked Up _____	Bibliographic _____	Dr. Link _____
Date Completed: <u>6/19</u>	Litigation _____	Lexis/Nexis _____
Searcher Prep & Review Time: <u>5</u>	Fulltext _____	Sequence Systems <u>CompuGen</u>
Clerical Prep Time _____	Patent Family _____	WWW/Internet _____
Online Time: <u>6</u>	Other _____	Other (specify) _____

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 18, 2001, 15:29:32 ; Search time 50.45 Seconds

(without alignments)
514.412 Million cell updates/sec

Title: US-09-653-755A-4

Perfect score: 2427

Sequence: 1 EVQIQQSPELVKKPGASVMI.....RHGILKNYIKTKTISRSPGK 454

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 390729 seqs, 57163235 residues

Total number of hits satisfying chosen parameters: 390729

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

A.GeneSeq_0401:*

1: /SID56/gcgdata/geneSeq/geneSeq/AA1980.DAT:*
2: /SID56/gcgdata/geneSeq/geneSeq/AA1981.DAT:*
3: /SID56/gcgdata/geneSeq/geneSeq/AA1982.DAT:*
4: /SID56/gcgdata/geneSeq/geneSeq/AA1983.DAT:*
5: /SID56/gcgdata/geneSeq/geneSeq/AA1984.DAT:*
6: /SID56/gcgdata/geneSeq/geneSeq/AA1985.DAT:*
7: /SID56/gcgdata/geneSeq/geneSeq/AA1986.DAT:*
8: /SID56/gcgdata/geneSeq/geneSeq/AA1987.DAT:*
9: /SID56/gcgdata/geneSeq/geneSeq/AA1988.DAT:*
10: /SID56/gcgdata/geneSeq/geneSeq/AA1989.DAT:*
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12: /SID56/gcgdata/geneSeq/geneSeq/AA1991.DAT:*
13: /SID56/gcgdata/geneSeq/geneSeq/AA1992.DAT:*
14: /SID56/gcgdata/geneSeq/geneSeq/AA1993.DAT:*
15: /SID56/gcgdata/geneSeq/geneSeq/AA1994.DAT:*
16: /SID56/gcgdata/geneSeq/geneSeq/AA1995.DAT:*
17: /SID56/gcgdata/geneSeq/geneSeq/AA1996.DAT:*
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19: /SID56/gcgdata/geneSeq/geneSeq/AA1998.DAT:*
20: /SID56/gcgdata/geneSeq/geneSeq/AA1999.DAT:*
21: /SID56/gcgdata/geneSeq/geneSeq/AA2000.DAT:*
22: /SID56/gcgdata/geneSeq/geneSeq/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1839.5	75.8	468	12	Monoclonal antibody
2	1835	75.6	469	14	Monoclonal antibody
3	1789.5	73.7	9	P83200	Sequence encoded b
4	1693.5	69.8	447	10	Chimeric antibody
5	1670.5	68.8	477	15	T84.12 Heavy chain
6	1594.5	65.7	464	16	Mab 55.1 heavy chain
7	1590.5	65.5	445	16	Mab 55.1 heavy chain
8	1564.5	64.5	464	19	Anti-Fas Mab HFE7A
9	1564.5	64.5	464	21	Mouse anti-Fas ant
10	1564.5	64.5	464	21	Mouse anti-Fas ant
11	1559	64.2	453	20	Antibody F19 chine

12	1550.5	63.9	472	20	Y50157
13	1550	63.9	465	16	R66758
14	1548	63.8	454	14	R30774
15	1493.5	61.5	470	21	B08026
16	1489.5	61.4	472	20	Y50166
17	1466.5	60.4	449	14	R43339
18	1466.5	60.4	449	19	W49816
19	1461.5	60.2	470	21	W90933
20	1459.5	60.1	470	21	W90934
21	1458.5	60.1	470	19	W83037
22	1458.5	60.1	470	21	B14779
23	1458.5	60.1	470	21	W90929
24	1458.5	60.1	470	21	W90935
25	1457.5	60.1	470	19	W83036
26	1457.5	60.1	470	21	B14776
27	1457.5	60.1	470	21	W90926
28	1456.5	60.0	652	19	W48650
29	1455.5	60.0	464	18	W14941
30	1455.5	60.0	464	18	W14938
31	1455.5	60.0	468	13	R28808
32	1451.5	59.8	481	13	R24442
33	1451.5	59.8	595	20	W86003
34	1447	59.6	467	22	B36210
35	1446	59.6	463	18	W14939
36	1446	59.6	463	18	W14940
37	1439.5	59.3	470	21	W90936
38	1434	59.1	448	14	R43673
39	1433	59.0	448	17	R73736
40	1429.5	58.9	468	20	W85689
41	1429.5	58.9	711	20	W85692
42	1427.5	58.8	476	14	R31023
43	1427	58.8	452	20	Y29458
44	1427	58.8	452	21	B30322
45	1427	58.8	452	21	Y77766

ALIGNMENTS

RESULT	ID	Standard	Protein	Length	AA
1	R13061				
	R13061	standard	Protein	468	AA.
	AC	R13061			
	DT	03-OCT-1991	(first entry)		
	DE	Monoclonal antibody OK3T	heavy chain.		
	XX	OK3T	light chain; humanised antibodies; CDR-grafting.		
	XX	Mus musculus.			
	XX	Mus musculus.			
	FT	Peptide	1..19		
	FT	Protein	20..468		
	FT		/label= light chain		
	PN	W09109967-A.			
	PD	11-JUL-1991.			
	PF	21-DEC-1990;	90WO-GH02017.		
	PR	21-DEC-1990;	90WO-GH02017.		
	PR	21-DEC-1989;	89GB-0028874.		
	PA	(CELL-) CELLTech LTD.			
	PI	Adair JR, Athwal DS, Emirage JS;			
	DR	WPI; 1991-222915/30.			

Chimeric mouse/hum
Anti-tobacco mosai
H52H4-160 murine a
A dimeric anti-CD2
Human reshaped F19
Completely humanis
Amino acid sequenc
Humanised anti-Fas
Humanised anti-Fas
Anti-Fas humanised
Humanised anti-Fas
Humanised HFE7A de
Humanised anti-Fas
Anti-Fas humanised
Humanised anti-Fas
Heavy chain of hma
3F4 Human IgG4 exp
Murine anti-porcini
pre-5A8 humanised
Sequence of antio
Anti-574 single ch
Human immune syste
3F4 (Chimeric) hum
3F4 (Chimeric) hum
Humanised HFE7A de
Mouse anti-bovine
Murine anti-BGH MA
D9D10 heavy chain
Morbilli fusion pro
Antibody D heavy c
Recombinant immu
Humanised anti-IL-
Humanised anti-IL-

CC	residue with a different side chain; 318 (changed to Val) 320 and
CC	332 (changed to Gln). Those with altered lytic properties, as
CC	compared with unmodified Ab may have an altered CH2 domain where
CC	residue 297 of the heavy chain has been changed to Ala.
XX	
SO	Sequence 341 AA:
	Query Match 73.7%; Score 1789.5; DB 9; Length 341;
	Best Local Similarity 98.5%; Pred. No. 2,6e-108;
	Matches 336; Conservative 0; Mismatches 0; Indels 5; Gaps
QY	119 AKTTPSVYVLAAGCGDGTSSSTVLGLCYKGRPESEVYVYTNMSSGISVHFFPALDSG 178
Db	1 aktpsvvplapgcqdltsvllgclvkgyfpevsvtlwmsgslssvhtfpallqsg 60
QY	179 LYTMSSSVTPPSSTWPSQQTGCVAHPASSTVYDKKLEPSGPISTINPCPKCECHKCPA 238
Db	61 lytmsssvtpssstcwpqqltscvavahpastvdkkklpsgpiistlnpcpkcechkcpa 120
QY	239 PNLGGPSVFIFPPNIDYLMISLTFRKVTGVYDVASEDDPDV----QISMFVNNVVEVHT 293
Db	121 pnlggpsviflfpnldkvlmisltpkvcvvydvasedpdrpdpqqlswfvnmvyrht 180
Db	294 AQGTQREDYNSTIRVYSTLPFIQHODMSSGKEFKCKVNNKDLPSPIERTISKIGLVRAAP 353
QY	354 QVYILPPPAQLSRKDYSLTCLVGVGNRPQDISVEMTSNQHTEENKQDPAVLDSSGSYFI 413
Db	241 qvylpppaqlsrkdslclclvvgtnpqlslvewtsnqhnteenykdtpavldsdgsyfi 300
QY	414 YSKLNMKTSKWEKTDSPSCNVHREGLKNNYLLKKTISRSPGK 454
Db	301 ysklnmktskwektdsfscnvrneglknnyllkktlstrspgk 341
RESULT 4	
XX	P93037
AC	P93037 standard; protein; 447 AA.
XX	P93037;
XX	14-MAR-1990 (first entry)
DT	
DE	Chimeric antibody heavy chain variable region.
OS	Mus.
XX	
XX	KSI/4; chimeric antibody; heavy chain variable region;
XX	EP338767-A.
PN	
XX	25-APR-1989.
DD	
XX	18-APR-1989; 89EP-0303814.
PF	
PR	21-APR-1988; 88US-0184522.
XX	
PA	(ELIL) ELI LILLY AND CO.
PA	
PI	Beavers LS, Bumol TF, Gadeki RA, Weigel BJ;
DR	WPI; 1989-311203/43.
DR	N-PSDB; N91659.
XX	
XX	Recombinant DNA cpds. producing antibodies - monoclonal and
PT	chimeric derived from monoclonal antibody KSI/4.
XX	
PS	Claim 6; page 50; 89pp; English.
XX	
XX	The sequence encodes the heavy chain of MAb KSI/4, used to
CC	construct mouse/human chimeric antibodies. KSI/4 is a murine antibody


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XX OS Mus sp.
XX FH Key
XX FT Peptide
XX FT /label= Sig-peptide
XX FT Protein
XX FT /label= Mat-protein
XX FT /note= "Claim 3, page 97-98"
XX PN WO9515382-A.
XX PD 08-JUN-1995.
XX PE 29-NOV-1994; 94WO-GB02610.
XX PR 03-JUN-1994; 94GB-0011089.
XX PR 03-DEC-1993; 93GB-0024819.
XX PA (ZENE ) ZENECA LTD.
XX PI Blakey DC, Boot C, Copley CG, Hall SM, Paterson DS;
XX PI Rose MS, Wright AF;
XX DR WPI: 1995-215262/28.
XX DR N-PsDB: Q94037.
XX PT Antigen binding structures containing CDRs recognising the CA55.1
XX PT antigen - produced by hybridomas and host cells, for use in the
XX PT diagnosis and therapy of cancer
XX PS Disclosure; Fig.15; 121pp; English.
XX CC MAb 55.1 (ECCACC 93081901) recognises the colorectal tumor-associated
XX CC antigen CA55.1. cDNAs for the heavy (Q94037) and light (Q94036)
XX CC chains of 55.1 were isolated, and F(ab)'2, F(ab)'2, Fv, scFv or
XX CC V-min humanized 55.1 constructs have been expressed in myeloma
XX CC cells and E. coli.
XX SQ Sequence 464 AA;

Query Match 65.7%; Score 1594.5; DB 16; Length 464;
Best Local Similarity 66.5%; Pred. No. 1.4e-95;
Matches 304; Conservative 55; Mismatches 83; Indels 15; Gaps 6;

QY 1 EVQLQSSPELVKPKASVMISCRSAVTFTENTYHWVKQSHGESLEWIGINPYGGSIF 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 20 qvqlqpggaellvkpgasvqlsckasgyftlgylwhvqrpqgglewlgenvpsstgrsdy 79
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 SPFKGKATLTVDKSSSTAYMELRLTSEDSAVYYCAR-RAGAY--YFDYWGQGTTLTVS 117
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 80 nekfkakcltvdksstlaymqlsltsedsavyycareraygyddandygqgsrvts 139
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 118 SAKTTPSPVPLAPGCGDTTSSVTLGCLVKGYPESTVTWNSGSLSSVHTPALLQS 177
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 140 sakttpspvplapgsaaqtsmvtlglclvkgyfpepvtlwnsgslssgyvhtfpavlg 199
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 178 GLYTMSSSVTPSSSTWPSQVTCSAVHAASSTYVDKRLPSGPISTINPCPCKCKHCP 237
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 200 dlylsssvtpssstwpsetlcnvahpasstikvdkiivp-----tdc-gckpc-ict 250
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 238 APNLEGGBSVFIFPPNKKIDVIMISLTFRKVTGVVVDSEDDPDVQISWENVNVEHTAQT 297
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 251 vpevs---svflfppkpkdviltltltpkvtcuvvdiskdpevgqswfvddevhlaqtq 307
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 298 THRSDYNTIVVSGTLPIQHDMMSGKEFKCKVNNKKDLPSPLERTISIKGLVRAAPQYI 357
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 308 preegfnstfsvseipumhgdwlngkefkcrvnsaafraplektsktkgrkapyvt 367
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 358 LPPPAEQLSRKDVSLTCLVGFNPGDISVEWTSNGHTEENKDPAPVADSDGSVFYISKL 417
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 368 lpppkqgmakakvalctmctdfpfeditvewqmgwngpaenyknqgrindtqgsyfvyskl 427
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

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QY 418 NMKTSKMEKTDSPFCNVNRHEGLKANYLLKKTISRSPGK 454
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 428 nvqksnweagntftscvslghhnhhteksishspgk 464

RESULT 7
ID R76085 standard; Peptide; 445 AA.
XX AC R76085;
XX DE 21-NOV-1995 (first entry)
XX DE MAb 55.1 heavy chain.
XX KW Antigen binding structure; complementarity determining region; CDR:
XX KW CA55.1; colorectal cancer; tumor-associated antigen; hybridoma;
XX KW monoclonal antibody; MAb; immunotherapy; therapy; diagnosis;
XX KW transgenic animal; transgenic plant; antibody engineering;
XX KW humanized antibody; immunotoxin.
XX OS Mus sp.
XX PN WO9515382-A.
XX PD 08-JUN-1995.
XX PE 29-NOV-1994; 94WO-GB02610.
XX PR 03-JUN-1994; 94GB-0011089.
XX PR 03-DEC-1993; 93GB-0024819.
XX PA (ZENE ) ZENECA LTD.
XX PI Blakey DC, Boot C, Copley CG, Hall SM, Paterson DS;
XX PI Rose MS, Wright AF;
XX DR WPI: 1995-215262/28.
XX PT Antigen binding structures containing CDRs recognising the CA55.1
XX PT antigen - produced by hybridomas and host cells, for use in the
XX PT diagnosis and therapy of cancer
XX PS Claim 3; Page 97-98; 121pp; English.
XX CC An antigen binding structure is based on the CDRs (given in R76078-
XX CC 84) of the heavy (R76085) and light (R76086) chains of MAb 55.1
XX CC (ECCACC 93081901), which recognises the colorectal tumor-associated
XX CC antigen CA55.1. It is optionally humanized and in the form F(ab)'2,
XX CC F(ab)'2, Fv, scFv or V-min, and is produced in transgenic
XX CC animals or plants.
XX SQ Sequence 445 AA;

Query Match 65.5%; Score 1590.5; DB 16; Length 445;
Best Local Similarity 66.5%; Pred. No. 2.5e-95;
Matches 304; Conservative 54; Mismatches 84; Indels 15; Gaps 6;

QY 1 EVQLQSSPELVKPKASVMISCRSAVTFTENTYHWVKQSHGESLEWIGINPYGGSIF 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 qvqlqpggaellvkpgasvqlsckasgyftlgylwhvqrpqgglewlgenvpsstgrsdy 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 SPFKGKATLTVDKSSSTAYMELRLTSEDSAVYYCAR-RAGAY--YFDYWGQGTTLTVS 117
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 nekfkakcltvdksstlaymqlsltsedsavyycareraygyddandygqgsrvts 120
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 118 SAKTTPSPVPLAPGCGDTTSSVTLGCLVKGYPESTVTWNSGSLSSVHTPALLQS 177
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 sakttpspvplapgsaaqtsmvtlglclvkgyfpepvtlwnsgslssgyvhtfpavlg 180
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 178 GLYTMSSSVTPSSSTWPSQVTCSAVHAASSTYVDKRLPSGPISTINPCPCKCKHCP 237
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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Qy	178	GLTMSSSVYPTSTWPSQVYTSVAHPSASTVYDKLLEPSPGISTININCPCKEHCRC	237
Db	200	dlylssslvlpstlpsqvtlcvahpssstlckllyp-----rdc-gkpc-ict	250
Qy	238	APNLEGGSYVFIFPPNPKIDVLMISLAPKVCYVVDVSEDDPVDQISMFVNNVEVHAQRC	297
Db	251	vpevs-----svtlfpbkxkvltltlfpkvcvvvdlskddpewgfsvfrddvevhaqg	307
Qy	238	THREDYNSTIRVSTLPIQHODMNSGKEPKCKVNNKDLPSPIERTISKIKGLVRAPOYVI	357
Db	308	preeflnstfsvselplmbqnwlngefkrcvnsaafpepliekltiskctkgrpkapqvt	367
Qy	358	LPPAEOLSRKDVSLTCLVYGFNPGDISVMTNLSGHEENYKQTAVALNDSGSFYISKL	417
Db	368	lpphkeqakakvslctmldlfpdeltlvwqyqpaenykntqplmngsytyvskl	427
Qy	418	NMKTSMKEKTDPSFCNVRHDEGLKNVYLKKTIRSPCK	454
Db	428	nvqksnweagntfcsvlhqglhnhhekslmspgk	464
RESULT	10		
W90897		W90897 standard; Protein; 464 AA.	
XX	AC	W90897;	
XX	DT	08-AUG-2000 (first entry)	
XX	DE	Murine anti-Fas antibody HFE7A heavy chain protein.	
XX	KM	Fas: antibody; murine; anti-inflammatory; anti-anemic; antidiabetic;	
XX	KM	anti-allergic; anti-arthritic; antiviral; immunomodulatory; cardiact;	
XX	KM	dematological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas	
XX	KM	neurotropic; antifertility; neuroprotective; antiarteriosclerotic;	
XX	KM	hepatotropic; humanized; apoptosis; systemic lupus erythematosus; HFE7A;	
XX	KM	Hasimoto disease; rheumatoid arthritis; graft versus host disease;	
XX	KM	Storgen's syndrome; anemia; Addison's disease; scleroderma; sterility;	
XX	KM	Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;	
XX	KM	multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;	
XX	KM	insulin dependent diabetes mellitus; arteriosclerosis; myocardiatis;	
XX	KM	cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.	
XX	OS	Mus musculus.	
XX	PN	EP990663-A2.	
XX	PD	05-APR-2000.	
XX	PE	29-SEP-1999; 99EP-0307711.	
XX	PR	30-SEP-1998; 98JP-0276881.	
XX	PR	30-SEP-1998; 98JP-0276882.	
XX	PA	(SANY) SANKYO CO LTD.	
XX	PI	Serizawa N, Hatuyama H, Nakahara K, Tamaki I, Takahashi T;	
XX	DR	WPI: 2000-258930/23.	
XX	DR	N-PSDB: A11546.	
XX	PT	New humanized anti-Fas antibody, useful for treating or preventing e.g.	
XX	PT	inflammatory or autoimmune disease, induces apoptosis selectively in	
XX	PT	cells with abnormal Fas-Fas ligand systems	
XX	PS	Example reference 4; Page 100-102; 263pb; English.	
XX	CC	This invention describes a novel humanized anti-Fas antibody-like	
XX	CC	molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas	
XX	CC	ligand system, by binding to Fas on the cell surface, and prevents	
XX	CC	apoptosis in cells with a normal system, by inhibiting binding between	
XX	CC	Fas and its ligand. The products of the invention have anti-inflammatory	

QY	176	Q-SGLYTMSSSVVPSPSTMSQVTCVSAHPASSTVDDKKLPESGISTINCPCKECH	234
QY	181	qsgslgyslsvsvtpssqlygtlyicnvhmkpntckvkvepkscdkt-hccpp-----	234
QY	235	KCPAPNIEGCPSEFIEPPFNKIDVIMLSTPRKYCVAVDVSEDDPVDQISMFNNEVHTA	294
Db	235	-cpapellgpsvflfpkpkcdtlmstrpctccvvvdshnedpevklmvydyevhna	293
QY	295	QQTQTHREDYNSTIRVSTLPDIQHODMWSGKEFKCKVNNKDLPSPIERTISIKIGLVRAQ	354
QY	355	VYLIPPAEQLSKRDVSLTCLVGVFNPRGDISVMTSNGHTENYKDTFAYLDSDSYFIY	414
Db	354	vyltppreemctknqysltclvkgyfypsdlavewesngpennyykltplvlsdgsffly	413
QY	415	SKLNMKTSKWEKTDPSFCNVHCEGLKNKYLLKRTISRSPGK	454
Db	414	skltvdksrhwggnvfscsymhalmhnytkqlsispqk	453
RESULT	12		
ID	Y50157		
AC	Y50157	standard; Protein; 472 AA.	
XX	Y50157;		
DE	31-JAN-2000	(first entry)	
KW	Chimeric mouse/human F19 antibody heavy chain.		
KW	Antibody; monoclonal; F19; fibrinogen activation protein alpha; FAP;		
KW	humanisation; complementarity determining region; CDR; CDR grafting;		
KW	reactive stroma; fibroblast; epithelial cancer; diagnosis;		
KW	immune response; framework sequence; constant region;		
KW	variable region; producibility; treatment; cancer; colorectal; lung;		
KW	breast; head; neck; ovarian; lung; bladder; pancreatic; metastasis;		
KW	detection; wound healing; skin inflammation; tumour; immunogenicity		
XX	chimeric; heavy chain.		
OS	Chimeric - Mus sp.		
XX	Chimeric - Homo sapiens.		
XX	Key	Location/Qualifiers	
FT	Peptide	1..19	
FT	Protein	/note= "leader peptide"	
FT	Region	20..472	
FT	Region	/note= "Mature chimeric mouse/human F19 heavy chain"	
FT	Region	20..143	
FT	Region	/note= "Mature mouse F19 heavy chain variable region"	
FT	Region	50..54	
FT	Region	/note= "Complementarity determining region (CDR) 1"	
FT	Region	69..85	
FT	Region	/note= "CDR 2"	
FT	Region	118..132	
FT	Region	/note= "CDR 3"	
FT	Misc-difference	143..144	
FT	FT	/note= "mRNA splicing causes an Ala to be inserted	
FT	FT	between these residues"	
FT	Region	144..472	
PN	EP953639-A1.	/note= "Human gamma-1 heavy chain constant region"	
PN	03-NOV-1999.		
XX	30-APR-1998;	98EP-0107925.	
XX	30-APR-1998;	98EP-0107925.	
XX	(BOEH) BOEHRINGER INGELHEIM INT GMBH.		
XX	Park JE, Garin-Chesa P, Bamberg U, Leger O, Saldanha J;		

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PI  Rettig WT,
XX  WPI: 1999-621833/54.
DR  N-PSDB: 232482.
XX
XX  New antibody protein, useful for treating cancer and for imaging
PT  presence of activated stromal fibroblasts in healing wound or inflamed
PT  skin -
XX
XX  Example 1; Fig 27; 143pp; English.
PS
XX
CC  This sequence represents the heavy chain of a chimeric mouse/human F19
CC  antibody. F19 (ATCC Accession number HB 8269) is a murine monoclonal
CC  antibody against fibroblast activation protein alpha (FAP). FAP is a cell
CC  surface molecule of reactive stromal fibroblasts, and its induction
CC  is a highly consistent molecular trait of the reactive stroma of many
CC  types of epithelial cancer. Although F19 may be useful in vitro, e.g.,
CC  for diagnosis, its applications for in vivo use in humans are problematic
CC  as it elicits a human anti-mouse response which reduces the efficacy of
CC  the antibody in patients and impairs continued administration. This
CC  chimeric antibody was humanised by joining entire murine variable regions
CC  to human constant regions. However, humanised antibodies produced by this
CC  method can still elicit an anti-mouse response in humans, whereas
CC  antibodies humanised via CDR (complementarity determining region)
CC  grafting are less immunogenic in humans. Humanised F19 antibodies are
CC  useful for treating cancers e.g., colorectal cancers, non-small cell
CC  lung cancers, breast cancers, head and neck cancers, ovarian cancers,
CC  lung cancers, bladder cancers, pancreatic cancers and metastatic cancers.
CC  They are also useful for the detection of activated stromal fibroblasts
CC  in a healing wound, inflamed skin or a tumour in a human patient.
XX
XX  Sequence 472 AA:
SQ
XX
XX  Query Match 63.9%; Score 1550.5; DB 20; Length 472;
XX  Best Local Similarity 64.4%; Pred. No. 1e-92; Mismatches 15; Gaps 5;
XX  Matches 297; Conservative 62; Indels 87;
XX
XX  1 EVQLQDSPELTKPPASVAVISCRATSYFTFNTVMVAKOSHSLEWIGINPYGGSIF 60
XX  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX  20 evqlqdspe|v|tkppasv|a|v|s|c|r|a|t|s|y|f|t|f|n|t|v|m|v|a|k|o|s|h|s|l|e|w|i|g|i|n|p|y|g|g|s|i|f| 79
XX
XX  61 SPKFKGATLVIVDKSSSPAYMELRSLSSEDSAVVYCCARRAGAYVF-----DYWGQGTTL 114
XX  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX  80 spkfkgrat|lv|vdkss|sp|a|y|m|e|l|r|s|l|s|e|d|s|a|v|v|y|c|c|a|r|r|a|g|a|y|v|f| 139
XX
XX  115 TVSSAKTRPPSYVPLAPGCGDTGSSVTLGLCLVKGTFPESYVYVWNNSSGLSSSVTFPAL 174
XX  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX  140 tvssaktrppsyv|plap|g|c|g|d|t|g|s|s|v|t|l|g|c|l|v|k|g|t|f|p|e|s|y|v|y|v|w|n|n|s|s|g|l|s|s|v|t|f|p|a|l| 198
XX  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX  175 LQ-SGLYTMSSSVYPPSSWMPQSOTVTCGSAVHAPASSTVWDKRLKPEPSGISTIRPCPKKCC 233
XX  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX  199 lqsgsllyalsvsvy|ppss|w|mp|q|s|o|t|v|t|c|g|s|a|v|h|a|p|a|s|s|t|v|w|d|k|r|l|k|p|e|p|s|g|i|s|t|i|r|p|c|k|k|c|c| 253
XX
XX  234 HKCPARNLEGGSVDFLPFNKIDVLMISLTPKVTGVVVDSEDDPVOVISWFVNNVYHT 293
XX  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX  254 --cp|a|r|n|l|e|g|g|s|v|d|f|p|f|n|k|i|d|v|l|m|i|s|l|t|p|k|v|t|g|v|v|d|s|e|d|d|p|v|o|i|s|w|f|v|n|n|v|y|h|t| 311
XX
XX  294 AQOTQHREDYNSTINVSITLPIQHDMMMSGKFKCKVNNKKDLPSLIERIKSLIKGLVAP 353
XX  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX  312 aqotqhredynst|invs|it|l|p|i|q|h|d|m|m|s|g|k|f|k|c|k|v|n|n|k|k|d|l|p|s|l|i|e|r|i|k|s|l|i|k|g|l|v|a|p| 371
XX
XX  354 QYIILPAPAEQDSRKDVSLTCLVWFENFGDISVENTSNQGTDEENKRDAPVLDSDGSYFI 413
XX  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX  372 qy|il|p|a|p|a|e|q|d|s|r|k|d|v|s|l|t|c|l|v|w|f|e|n|f|g|d|i|s|e|n|t|s|n|q|g|t|d|e|e|n|k|r|d|a|p|v|l|d|s|d|g|s|y|f|i| 431
XX
XX  414 YSKLNMKTSKWEKTDTSFCNVNRHEGLKNVYLYKTLISRSBPK 454
XX  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX  432 yskl|t|v|d|k|s|r|w|g|q|n|v|f|a|s|c|v|h|e|a|l|h|n|h|y|t|q|t|s|l|s|p|g|k| 472
XX
XX  RESULT 13
XX  966758

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